Figure 2

T7 promoter

AGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAATTCCCC

RBS

TCTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATATACC

NdeI

ATGGGCAGCAGCCATCATCATCATCATCACAGCAGCGGCCTGGTGCCGCGCGGCAGC**CATATG**GGATCC

GG

M G S S H H H H H H S S G L V P R G S H M ------

--

StuI   SalI

AATTCAAAGGCCTAC**GTCGAC**TAGAGCCTGCAGT*CTCGA*CCATCATCATCATCATCATTAATAAAAGGG

CG

---------------------- *

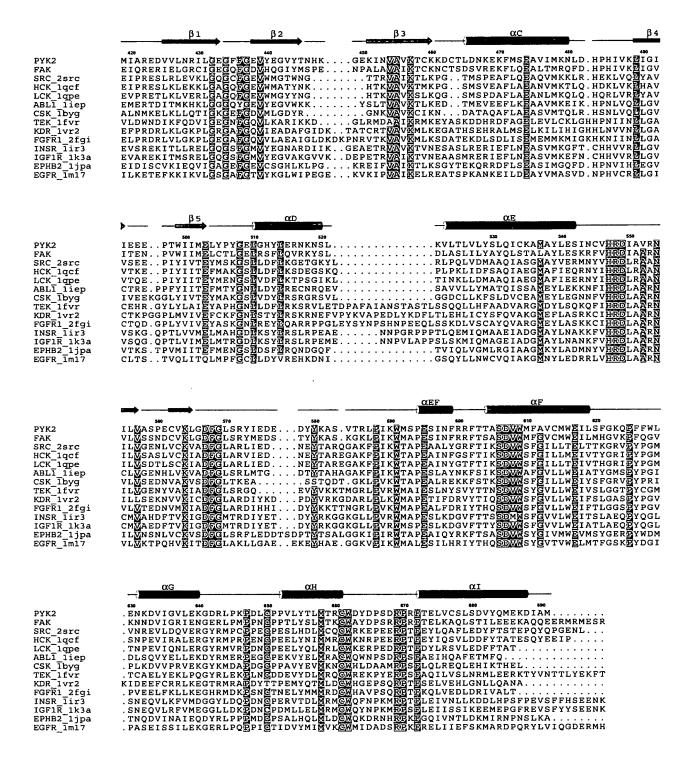**SpeI BamHI**

AATTCCAGCACACTGGCGGCCGTT**ACTAGT**GGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTT

GG

  IVEX-3 Primer

Bpu1102 I   **T7 terminator**

CTGCTGCCACCGCTGAGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTT

TG

          3'-PET Primer

Figure 3

β1 β2 β3 αC β4

```
                420        430        440            450        460        470        480         490
PYK2        MIAREDVVLNRILGEGFFGEVYEGVYTNHK....GEKINVAVKTCKKDCTLDNKEKFMSEAVIMKNLD.HPHIVKLIGI
FAK         EIQRERIELGRCIGEGQFGDVHQGIYMSPE....NPALAVAIKTCKNCTSDSVREKFLQEALTMRQFD.HPHIVKLIGV
SRC_2src    EIPRESLRLEVKLGQGCFGEVWMGTWNG.......TTRVAIKTLKPG..TMSPEAFLQEAQVMKKLR.HEKLVQLYAV
HCK_1qcf    EIPRESLKLEKKLGAGQFGEVWMATYNK.......HTKVAVKTMKPG..SMSVEAFLAEANVMKTLQ.HDKLVKLHAV
LCK_1qpe    EVPRETLKLVERLGAGQFGEVWMGYYNG.......HTKVAVKSLKQG..SMSPDAFLAEANLMKQLQ.HQRLVRLYAV
ABL1_1iep   EMERTDITMKHKLGGGQYGEVYEGVWKK.......YSLTVAVKTLKED..TMEVEEFLKEAAVMKEIK.HPNLVQLLGV
CSK_1byg    ALNMKELKLLQTIGKGEFGDVMLGDYR.........GNKVAVKCIKN...DATAQAFLAEASVMTQLR.HSNLVQLLGV
TEK_1fvr    VLDWNDIKFQDVIGEGNFGQVLKARIKKD.....GLRMDAAIKRMKEYASKDDHRDFAGELEVLCKLGHHPNIINDLGA
KDR_1vr2    EFPRDRLKLGKPLGRGAFGQVIEADAFGIDK..TATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHLNVVNLLGA
FGFR1_2fgi  ELPRDRLVLGKPLGEGAFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIINLLGA
INSR_1ir3   EVSREKITLLRELGQGSFGMVYEGNARDIIK..GEAETRVAVKTVNESASLRERIEFLNEASVMKGFT.CHHVVRLLGV
IGF1R_1k3a  EVAREKITMSRELGQGSFGMVYEGVAKGVVK..DEPETRVAIKTVNEAASMRERIEFLNEASVMKEFN.CHHVVRLLGV
EPHB2_1jpa  EIDISCVKIEQVIGAGEFGEVCSGHLKLPG....KREIFVAIKTLKSGYTEKQRRDFLSEASIMGQFD.HPNVIHLEGV
EGFR_1m17   ILKETEFKKIKVLGSGAFGTVYKGLWIPEGE...KVKIPVAIKELREATSPKANKEILDEAYVMASVD.NPHVCRLLGI
```

β5 αD αE

```
                       500        510        520              530        540        550
PYK2        IEEE..PTWIIMELYPYGEIGHYLERNKNSL...............KVLTLVLYSLQICKAMAYLESINCVHRDIAVRN
FAK         ITEN..PVWIIMELCTLGEIRSFLQVRKYSL...............DLASLILYAYQLSTALAYLESKRFVHRDIAARN
SRC_2src    VSEE..PIYIVTEYMSKGSLLDFLKGETGKYL...............RLPQLVDMAAQIASGMAYVERMNYVHRDLRAAN
HCK_1qcf    VTKE..PIYIITEFMAKGSLLDFLKSDEGSKQ...............PLPKLIDFSAQIAEGMAFIEQRNYIHRDLRAAN
LCK_1qpe    VTQE..PIYIITEYMENGSLVDFLKTPSGIKL...............TINKLLDMAAQIAEGMAFIEERNYIHRDLRAAN
ABL1_1iep   CTRE.PPFYIITEFMTYGNLLDYLRECNRQEV...............SAVVLLYMATQISSAMEYLEKKNFIHRDLAARN
CSK_1byg    IVEEKGGLYIVTEYMAKGSLVDYLRSRGRSVL...............GGDCLLKFSLDVCEAMEYLEGNNFVHRDLAARN
TEK_1fvr    CEHR.GYLYLAIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQFIHRDLAARN
KDR_1vr2    CTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKVAPEDLYKDFLTLEHLICYSFQVAKGMEFLASRKCIHRDLAARN
FGFR1_2fgi  CTQD.GPLYVIVEYASKGNLREYLQARRPPGLEYSYNPSHNPEEQLSSKDLVSCAYQVARGMEYLASKKCIHRDLAARN
INSR_1ir3   VSKG.QPTLVVMELMAHGDLKSYLRSLRPEAE....NNPGRPPPTLQEMIQMAAEIADGMAYLNAKKFVHRDLAARN
IGF1R_1k3a  VSQG.QPTLVIMELMTRGDLKSYLRSLRPEME.....NNPVLAPPSLSKMIQMAGEIADGMAYLNANKFVHRDLAARN
EPHB2_1jpa  VTKS.TPVMIITEFMENGSLDSFLRQNDGQF...............TVIQLVGMLRGIAAGMKYLADMNYVHRDLAARN
EGFR_1m17   CLTS..TVQLITQLMPFGCLLDYVREHKDNI...............GSQYLLNWCVQIAKGMNYLEDRRLVHRDLAARN
```

αEF αF

```
                       560        570        580        590        600        610        620
PYK2        ILVASPECVKLGDFGLSRYIEDE...DYYKAS.VTRLPIKWMSPESINFRRFTTASDVWMFAVCMWEILSFGKQPFFWL
FAK         VLVSSNDCVKLGDFGLSRYMEDS...TYYKAS.KGKLPIKWMAPESINRRFTSASDVWMFGVCMWEILMHGVKPFQGV
SRC_2src    ILVGENLVCKVADFGLARLIED....NEYTARQGAKFPIKWTAPEAALYGRFTIKSDVWSFGILLTELTTKGRVPYPGM
HCK_1qcf    ILVSASLVCKIADFGLARVIED....NEYTAREGAKFPIKWTAPEAINFGSFTIKSDVWSFGILLMEIVTYGRIPYPGM
LCK_1qpe    ILVSDTLSCKIADFGLARLIED....NEYTAREGAKFPIKWTAPEAINYGTFTIKSDVWSFGILLTEIVTHGRIPYPGM
ABL1_1iep   CLVGENHLVKVADFGLSRLMTG...DTYTAHAGAKFPIKWTAPESLAYNKFSIKSDVWAFGVLLWEIATYGMSEYPGI
CSK_1byg    VLVSEDNVAKVSDFGLTKEA......SSTQDT.GKLPVKWTAPEALREKKFSTKSDVWSFGILLWEIYSFGRVPYPRI
TEK_1fvr    ILVGENYVAKIADFGLSRGQ.....EVVKKTMGRLPIKWMAIESLNYSVYTTNSDVWSYGVLLWEIVSLGGTPYCGM
KDR_1vr2    ILLSEKNVVKICDFGLARDIYKD...PDYVRKGDARLPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSLGASPYPGV
FGFR1_2fgi  VLVTEDNVMKIADFGLARDIHHI...DYYKKTTNGRLPVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGV
INSR_1ir3   CMVAHDFTVKIGDFGMTRDIYET...DYYRKGGKGLLPVRWMAPESLKDGVFTTSSDMWSFGVVLWEITSLAEQPYQGL
IGF1R_1k3a  CMVAEDFTVKIGDFGMTRDIYET...DYYRKGGKGLLPVRWMSPESLKDGVFTTYSDVWSFGVVLWEIATLAEQEYQGL
EPHB2_1jpa  ILVNSNLVCKVSDFGLSRFLEDDTSDPTYTSALGGKIPIRWTAPEAIQYRKFTSASDVYSYGIVMWEVMSYGERPYWDM
EGFR_1m17   VLVKTPQHVKITDFGLAKLLGAE..EKEYHAE.GGKVPIKWMALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGI
```

αG αH αI

```
                       630        640        650        660        670        680        690
PYK2        .ENKDVIGVLEKGDRLPKPDLCPPVLYTLMTRGWDYDPSDRPRFTELVCSLSDVYQMEKDIAM........
FAK         .KNNDVIGRIENGERLPMPPNCPPTLYSLMTKGWAYDPSRRPRFTELKAQLSTILEEEKAQQEERMRMESR
SRC_2src    .VNREVLDQVERGYRMPCPEGCPESLHDLMCQGWRKEPEERPTFEYLQAFLEDYFTSTEPQYQPGENL...
HCK_1qcf    .SNPEVIRALERGYRMPRPENCPEELYNIMMRGWKNRPEERPTFEYIQSVLDDFYTATESQYEEIP.....
LCK_1qpe    .TNPEVIQNLERGYRMVRPDNCPEELYQLMRLGWKERPEDRPTFDYLRSVLEDFFTAT.............
ABL1_1iep   .DLSQVYELLEKDYRMERPEGCPEKVYELMRACGWQWNPSDRPSFAEIHQAFETMFQ..............
CSK_1byg    .PLKDVVPRVEKGYKMDAPDGCPPAVYEVMKNCGWHLDAAMRESFLQLREQLEHIKTHEL...........
TEK_1fvr    .TCAELYEKLPQGYRLEKPLNCDDEVYDLMRQGWREKPYERPSFAQILVSLNRMLEERKTYVNTTLYEKFT
KDR_1vr2    KIDEEFCRRLKEGTRMRADYTTPEMYQTMLDGWHGEPSQRPTFSELVEHLGNLLQANA.............
FGFR1_2fgi  .PVEELFKLLKEGHRMDKPSNCTNELYMMMRDGWHAVPSQRPTFKQLVEDLDRIVALT.............
INSR_1ir3   .SNEQVLKFVMDGGYLDQPDNCPERVTDLMRMGWQFNPKMRPTFLEIVNLLKDDLHPSFPEVSFFHSEENK
IGF1R_1k3a  .SNEQVLRFVMEGGLLDKPDNCPDMLLELMRMGWQYNPKMRPSFLEIISSIKEEMEPGFREVSFYYSEENK
EPHB2_1jpa  .TNQDVINAIEQDYRLPPPMDCPSALHQLMLDGWQKDRNHRPKFGQIVNTLDKMIRNPNSLKA........
EGFR_1m17   .PASEISSILEKGERLPQPPICTIDVYMIMVKGWMIDADSRPKFRELIIEFSKMARDPQRYLVIQGDERMH
```

Figure 4

4A:

```
  1 MGSSHHHHHH SSGLVPRGSH MIAREDVVLN RILGEGFFGE VYEGVYTNHK GEKINVAVKT
 61 CKKDCTLDNK EKFMSEAVIM KNLDHPHIVK LIGIIEEEPT WIIMELYPYG ELGHYLERNK
121 NSLKVLTLVL YSLQICKAMA YLESINCVHR DIAVRNILVA SPECVKLGDF GLSRYIEDED
181 YYKASVTRLP IKWMSPESIN FRRFTTASDV WMFAVCMWEI LSFGKQPFFW LENKDVIGVL
241 EKGDRLPKPD LCPPVLYTLM TRCWDYDPSD RPRFTELVCS LSDVYQMEKD IAM
```

4B:

PYK2-C1;   5'-TCCACAG CATATG ATTGCCCGTGAAGATGTGGT-3'   33 mer

4C:

PYK2-N2;   TGGAGAAGGACATTGCCATG TAG GTCGAC GAGAG (Origin)
              5'-CTCTC GTCGAC CTA CATGGCAATGTCCTTCTCCA-3'   34 mer

4D:

```
                                   TCTAGAAATAATTTTGTTTAACTTTAAGAAGGAGA

TATACCATGGGCAGCAGCCATCATCATCATCATCACAGCAGCGGCCTGGTGCCGCGCGGCAGCCATATG
          attgcc cgtgaagatg
1381 tggtcctgaa tcgtattctt ggggaaggct tttttgggga ggtctatgaa
ggtgtctaca
1441 caaatcacaa aggggagaaa atcaatgtag ctgtcaagac ctgcaagaaa
gactgcactc
1501 tggacaacaa ggagaagttc atgagcgagg cagtgatcat gaagaacctc
gaccacccgc
1561 acatcgtgaa gctgatcggc atcattgaag aggagcccac ctggatcatc
atggaattgt
1621 atccctatgg ggagctgggc cactacctgg agcggaacaa gaactccctg
aaggtgctca
1681 ccctcgtgct gtactcactg cagatatgca aagccatggc ctacctggag
agcatcaact
1741 gcgtgcacag ggacattgct gtccggaaca tcctggtggc ctcccctgag
tgtgtgaagc
1801 tgggggactt ggtctttcc cggtacattg aggacgagga ctattacaaa
gcctctgtga
1861 ctcgtctccc catcaaatgg atgtccccag agtccattaa cttccgacgc
ttcacgacag
1921 ccagtgacgt ctggatgttc gccgtgtgca tgtgggagat cctgagcttt
gggaagcagc
1981 ccttcttctg ctggagaac aaggatgtca tcggggtgct ggagaaagga
gaccggctgc
2041 ccaagcctga tctctgtcca ccggtccttt ataccctcat gacccgctgc
tgggactacg
2101 accccagtga ccggccccgc ttcaccgagc tggtgtgcag cctcagtgac
gtttatcaga
2161 tggagaagga cattgccatg
TAGGTCGACTAGAGCCTGCAGTCTCGACCATCATCATCATCATCATTAATAAAAGGGCG

AATTCCAGCACACTGGCGGCCGTTACTAGTGGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTT

GG
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